AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning on page 1, line 4 with the following replacement paragraph.

This application claims priority under 35 U.S.C. §120 to U.S. Patent Application No. 09/704,707, filed November 3, 2000 and under 35 U.S.C. §119(e) to U.S. Provisional Applications 60/202,027, filed May 4, 2000, 60/222,344, filed August 1, 2000, and 60/285,493, filed April 19, 2001, which are herein incorporated by reference in their entirety.

Please replace the paragraph beginning on page 6, line 18, with the following replacement paragraph:

Figures 1A-C indicates that mrgs define a Novel G protein-couple receptor Gene Family. Amino acid sequences of eight mouse full-length *mrg* genes were aligned using ClustalW. Identical residues in >50% of the predicted proteins are darkly shaded; conservative substitutions are highlighted in light gray. The approximate locations of predicted transmembrane domain 1-7 are indicated on top of the sequences as TM1-TM7. The predicted extracellular and cytoplasmic domains are indicated as E1-E7 and C1-C7 respectively.

Please replace the paragraph beginning on page 19, line 21 with the following replacement paragraph:

The "extracellular domain" (ECD) is a form of the Mrg or drg-12 receptor which is essentially free of the transmembrane and cytoplasmic domains, i.e., has less than 1% of such domains, preferably 0.5 to 0% of such domains, and more preferably 0.1 to 0% of such domains. Ordinarily, the ECD will have an amino acid sequence having at least about 60% amino acid sequence identity with the amino acid sequence of one or more of the ECDs of a native Mrg or drg-12 protein, for example as indicated in FIGS. 1A-C for mrg3 (E1, E2 etc...), preferably at least about 65%, more preferably at least about 75%, even more preferably at least about 80%, even more preferably at least about 90%, with increasing preference of 95%, to at least 99% amino acid sequence identity, and finally to 100% identity, and thus includes polypeptide variants as defined below.

Please replace the paragraph beginning on page 88, line 13 with the following replacement paragraph:

Among the novel genes isolated from the screen were two independent clones encoding a receptor protein with 7 transmembrane segments (SEQ ID NO: 1), a characteristic of G protein-coupled receptors. The novel 7 transmembrane receptor isolated is most closely related to the oncogene *mas*, and therefore has been named *mas-related gene-3 (mrg3)*. *mrg3* is also known as *mas-related gene A1*, or *MrgA1*. A complete coding sequence for *mrg3* has been deduced from the genomic DNA sequence (Figs. 1A-C and SEQ ID NO: 2). *MrgA1* shows significant homology (35% identity) to MAS1 (Young et al. Cell *45*: 711-9 (1986)). It also shares significant homology (30-35% identity) with two other mammalian GPCRs, called Mas-related gene 1 (MRG1) (Monnot et al. Mol Endocrinol *5*: 1477-87 (1991)) and rat thoracic aorta (RTA) (Ross et al. Proc Natl Acad Sci U S A *87*: 3052-6 (1990)).